

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT
CCAGAAAACAACCCCTTTTGTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCCCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCAGTCTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFI~~F~~SYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQM~~Q~~PKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSF~~F~~GGFLTYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCCTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGTGATCCTGG
TTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTCTTCTGGAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTGGTGTGTCAACTGCCCATACTTACATGCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGATAACA
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTGGTT
ACTTTTTCTCTATTTACTGTGTTTGAAAATTTTCATGGCTACCATCAATATTGTTTTGTATCGAGTT
GGGAAAACGGATCCTGTCACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTGGTCCCAACACATTTCCCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAAGTGCAGTTCAACTTCTATCACCCTGGTTTG
ATGTGATCTTCTGTCAGCGCTCTCTCTAGCATACTCTTCCCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA
GATATAAGAGGGGGGAAAATGGAACCAGGCGCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
ATTTTTACCTTCATAGCATACTCCTTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTAATCAGAGACTGTAACAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGCCGCCATGGCCCACTTGTTTATGAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV
LNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFFWKL GDP
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ
TMDMIISKKRMAMARRTMFQKGEVHNKPSGFWMIKSVTTSASGSENLTLIQQEVDAL EELSRQ
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTD PVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGATGGATTCTGGTTCATCTCTAG
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTGGGAAGGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
 ATTATCACCACCAAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACAGAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCCTACTACTCTCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAGTTTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAAAGCAGCATTCAAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGTCTCTCTCTTTTGGTGCTG
 CAGCTGGTCTTGGATTTTCTATGTCAAAGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAAAT
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA
 TGAGGAATCAAAGAAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC
 GATGCCCTGGAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
 CATGCTCCTTACCCTGCCCGAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA
 CCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAAT
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCT
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGAAGGAC
 CTAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGGTGGGTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGTAAGAGCAAAAGAAAT
 GGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAACTCTTATAAATTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAGTGCC
 ATTAACAAATGTACTAGCCCTCCTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

FIGURE 6

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGVVDGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFFPTNKNQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCCGG
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGCGCCGCGAGCGCAACTCGGTCCAGTCCGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCGCG
GCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTATGAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC
TGGACAAATGGTCTTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGGCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCTGTGTGC
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTGTGCAATTTGTTAGCT
CCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAACTGCA
GGAGCAGTTTGGCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTTGATAATTGTTTGGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAATG
CAACAAATGAATTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGG
AGGGGTCATTGTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACAGCCTTGGTGCCACCAAAAGTGTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTGAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCAGCAAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTATGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHL
RSVEEMEAEAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTGMVFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMCLTRDSECCGDQLCVWGH
TKMATRGSNGTICDNQRDCQPGLCFAFQRLFPVCTPLPVEGELCHDPASRLDLITWELEPDG
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQELEDLE
RSLTEEMALGEPAAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCACCTTGTGAACCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCCT
AACTGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAGATAGCCCGGTTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTCTGCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGGCTCCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAATAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAACAAAACAAACAAACAAA
AAGATTTTATTAAAGATATTTTGTTAACTC

FIGURE 10

RTGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGFWTL
NWVLALGQCVLAFASFYWAFHKPDPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAKNAFMLLMRN
IVRVVVLDKVTDLLLFFGKLLVVGGVVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

	1980	1979	1978	1977	1976	1975	1974	1973	1972	1971	1970	1969	1968	1967	1966	1965	1964	1963	1962	1961	1960	1959	1958	1957	1956	1955	1954	1953	1952	1951	1950	1949	1948	1947	1946	1945	1944	1943	1942	1941	1940	1939	1938	1937	1936	1935	1934	1933	1932	1931	1930	1929	1928	1927	1926	1925	1924	1923	1922	1921	1920	1919	1918	1917	1916	1915	1914	1913	1912	1911	1910	1909	1908	1907	1906	1905	1904	1903	1902	1901	1900	1899	1898	1897	1896	1895	1894	1893	1892	1891	1890	1889	1888	1887	1886	1885	1884	1883	1882	1881	1880	1879	1878	1877	1876	1875	1874	1873	1872	1871	1870	1869	1868	1867	1866	1865	1864	1863	1862	1861	1860	1859	1858	1857	1856	1855	1854	1853	1852	1851	1850	1849	1848	1847	1846	1845	1844	1843	1842	1841	1840	1839	1838	1837	1836	1835	1834	1833	1832	1831	1830	1829	1828	1827	1826	1825	1824	1823	1822	1821	1820	1819	1818	1817	1816	1815	1814	1813	1812	1811	1810	1809	1808	1807	1806	1805	1804	1803	1802	1801	1800	1799	1798	1797	1796	1795	1794	1793	1792	1791	1790	1789	1788	1787	1786	1785	1784	1783	1782	1781	1780	1779	1778	1777	1776	1775	1774	1773	1772	1771	1770	1769	1768	1767	1766	1765	1764	1763	1762	1761	1760	1759	1758	1757	1756	1755	1754	1753	1752	1751	1750	1749	1748	1747	1746	1745	1744	1743	1742	1741	1740	1739	1738	1737	1736	1735	1734	1733	1732	1731	1730	1729	1728	1727	1726	1725	1724	1723	1722	1721	1720	1719	1718	1717	1716	1715	1714	1713	1712	1711	1710	1709	1708	1707	1706	1705	1704	1703	1702	1701	1700	1699	1698	1697	1696	1695	1694	1693	1692	1691	1690	1689	1688	1687	1686	1685	1684	1683	1682	1681	1680	1679	1678	1677	1676	1675	1674	1673	1672	1671	1670	1669	1668	1667	1666	1665	1664	1663	1662	1661	1660	1659	1658	1657	1656	1655	1654	1653	1652	1651	1650	1649	1648	1647	1646	1645	1644	1643	1642	1641	1640	1639	1638	1637	1636	1635	1634	1633	1632	1631	1630	1629	1628	1627	1626	1625	1624	1623	1622	1621	1620	1619	1618	1617	1616	1615	1614	1613	1612	1611	1610	1609	1608	1607	1606	1605	1604	1603	1602	1601	1600	1599	1598	1597	1596	1595	1594	1593	1592	1591	1590	1589	1588	1587	1586	1585	1584	1583	1582	1581	1580	1579	1578	1577	1576	1575	1574	1573	1572	1571	1570	1569	1568	1567	1566	1565	1564	1563	1562	1561	1560	1559	1558	1557	1556	1555	1554	1553	1552	1551	1550	1549	1548	1547	1546	1545	1544	1543	1542	1541	1540	1539	1538	1537	1536	1535	1534	1533	1532	1531	1530	1529	1528	1
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[illegible]

FIGURE 12

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLLFTFFFLGLVLSIIMLSPGVESQL
YKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY
SFFHFCVLVSLHVMMLTNWYKPGETRMISTWTAVWVKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTTGTACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCGCCATTGGTGCGCAATAGCGTTGACAACGGCAGTGACCAGTGCCCTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGTGCCCATCATTTTCATTCATC
CTTGCTGGATTGAGACGTGGTTCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTTCCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTAAATGTGAAAAACCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTCAATTCAC
AGAAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTTCTTGTGTTTGCATTATGTGTATGGCCTGAAGTGTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTATATCATGTTTCCTTTGCGTTTCAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLQPQEAEEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGACCCGCCAGGAAAGACTGAGG
 CCGCGGCCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAGATGTGCTCCAG
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGACAGGGCTGCCCAT
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCGCCAGGGGACACGGTGCCC
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
 AGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCC
 TGCCAGCGGGGTCTTCCAGCCACTCGCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
 CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCGCCTGCTGCTGCTGGACCTCAGC
 CACAACACCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
 GGTGCTGCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
 TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCCTGACG
 CGCCTGCGGCTGGCCGGCAACCCCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGC
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
 TCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGC
 TGTGTTGGCCCTGGGTGCGGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCA
 CTTCGCCGCCAAGAACGCTGGCCGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG
 CCACCACCACCAGCCACAGTGGCCACCAGAGGCCGCTGGTGCGGGAGGCCACAGCCTTGCTCT
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCCCTC
 CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
 ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACG
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAG
 GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTATCGCAACCTATCG
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA
 GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCCGGCGGGTGCCGGAGG
 GCGAGGAGGCTGCGGGGAGGCCCATACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
 CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
 GCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGGGGGCGGCCATGGCAGCAGCGGCTCAGG
 ACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTCCCTTGGAG
 CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGTCTGAGTGTGAGGTGCC
 ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAAAGCCCTACATCTAAGCCA
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
 GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
 CTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
 CTTGGGCACGGCGGGGCTGCCATGTGCTGGTAACGCATGCCGCGTCTGCTGGGCTCTCCAC
 TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAAGGAAGATGC
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTATTTCT
 GGGAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTTGTAAGACAACCATGATATGAA
 GGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP LLLPL LLL L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P G P K A T E G G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTCAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAG
AAGATATCAGCTTTCTAGAGTCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCTTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAATGGAATGAAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTTGAAGAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
CTTCTGTATGCCTCTGGACTTGGTGTTAATCAAGTCAGGCAAAGGCTCTTGTATATTATACAT
TTGGAGCTCTTGGGGGAATCTAATAGCCACATGGTTTTGGTAAGTAGACTTTAGTGGAAGGCT
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTTTTCAGCTTTCATGATC
CAGATTTGCTTGTTAATTAAGACCAAATATTCAGTTGAACCTCCTTCAAATCTTGTTAATGGATAT
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCCATAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
AAATTTTGTAAATGGTGGCTATAGAAAACAACATGAAATATTATACAATATTTTGCAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG
TTTTTTACTTTTCATGATTGGCTGTCTTCCCATTTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGG
AAGATTAACTCATTTTAAATAAAATTATGTCTAAGATTAAAAA
AAA

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPFLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKKGFCETEEAAKRRQMQEAEEMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERVSYALLFGDYL PQNIQAAREMF EKLTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTTFGALGGNLI AHMVLVSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCCTGCAGTGGAATTTTCATGAAC TAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAAC TAAAGATTGAAGACATCACTG
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAAC TTTTGAT
AAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGTCTCTGGGGTCTGATCAATAATGCTGGTGTT
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGGAAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAACAAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAA
AGTCTAGACAAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKG FHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTNLMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFND SLRRDMK
AFGVHVSCIEPGLFKTNLADPVKVIIEKKLAIWEQLSPDIKQYGEGYIEKSLDKLKG NKSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTAGAAATATATCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATCCGT
CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTGCAGGAGCATTT
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTCCCTATATAAACCTCAAAAAGGACTTTTTTCACAGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACTGGGTATAAACTGTATCAGGTTCCGTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA
GAAAAGGAGAGGAGCACAGATTAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGA
ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATTCTGAATTTCTTCATTATGTGTT
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTTGATCCTTTTAAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC
TGTTTGCAGTAATACACAGATAACTCTTAGTGATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGGAAGGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAATAAATAAATGGAAGCAAGAATAGCCTTATTTCAAATATGGAAA
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIITESCSTHRLEHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV
QTHSSKFFEEGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSFLHSCVMSLKNRHVSKSSCYNHHLVDVNLTL
MVEHTDIPEASPASTPQIIKHKALDLDLRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCAA
GCAGCGCGCAGCGAACGCCCGCCGCCGCCACACCTCTGCGGTCCCCGCGGCGCTGCCACCTTCCCTCCTTCCCC
GCGTCCCCGCTCGCGGCCAGTCAGCTTGGCGGGTTCGCTGCCCCGCGAAACCCGAGGTACCAGCCCGCGCTCT
GCTTCCCTGGGCGCGCGGCCCTCCAGCCCTCCTTCTCCCTGGCCCGCGCTGGCACCAGGGGACCGTTGCCTGA
CGCGAGGCCAGCTCTACTTTTCCCCCGCTCTCTCGCCCTGCTCGCTCTTCCACCAACTCCAACCTCTCTCCC
TCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCGTAGCGCCGCTTCCCGTCCGGTCCCAA
GGTGGGAACGCGTCCGCCCCGGCCCGCACCATGGCAGCGTTGCGCTTGGCCGCGCTTCTCTGCACCTGGCAGTGCTC
AGCGCGCGCTGCTGGTGGCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCACGCTCTTACGTGTCAAAGGCTTC
AACAGAACGATGCCCCCTCCAGAGATCAACGGTGATCATTTGAAGATCTGTCCCCAGGGTTCTACCTGCTGCTCT
CAAGAGATGGAGGAGAAGTACAGCTGCAAAAGTAAAGATGATTTCAAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
CAAGCTGTCTTTGCTTACGTTACAAGAGTTTGATGAATTCTTCAAAGAACTACTTGAAGATGCAGAGAAATCCCTG
AATGATATGTTGTGAAGACATATGCCATTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATG
TTCGCGCTGGTGAACCTCCAGTACCATTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGAGCAGCTGAAG
CCCTTCGGAGATGCTCCTCGCAAATTGAAGCTCCAGGTACTCGTGCTTTTGTAGCAGCCGCTACTTTCGCTCAAGGC
TTAGCGGTTGCGGGAGATGCTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTGAAG
ATGATCTACTGCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACTACTGCTCAAACATCATGAGAGGC
TGTTTGGCAACCAAGGGATCTCGATTTTGAATGAACAATTTATAGATGCTATGCTGATGTTGGCAGAGAGGCTA
GAGGGTCTTTCAACATTGAATCGGTATGAGTCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
AATAGTGTTCAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
TCCATCTCTGAAAGTGCTTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACCACAGCAGCTGGCACT
AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCCTTCGAGCAAC
GTTTGAACGATGAGAGGATGGTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
CTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACCAGAC
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA
CAGGCTACCTCCTCACTGCTCTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATAATTCTCAAACCTCTGAG
AAAAAGTGTTTCATCAAAAAGTTAAAGGCACAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
TGGACAACAATGTACAGTTTTTACTATGTGGCACTGTTTAAAGAGTGTGACTTTGTTTTCTCATTCAGTTTTGGG
AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
CTATAGTTAGTTGTGATTGTGATTTATCACTCTATTATTTGTTGTATGTTTTTTCTCATTTGTTTTGTGGGT
TTTTTTTCCAACGTGTGATCTCGCTTGTTCCTTACAAGCAACAGGGTCCCTTCTTGGCAGTAACATGTACGTATT
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQGC GPPKPLPAGRISRSESASFARSFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACCTCACTCTCCCCTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLSSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTG
CTCTGTGCAGAGCCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTC
GAGCCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTA
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC
CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLPPLHMLALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL
TGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRLRPGGVLEFFWEHVAEPYGSWAFMWQOVFEPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSKALICSFPSL
QLEQATHQPIYLPRLGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

[illegible]

1954-55	1955-56	1956-57	1957-58	1958-59	1959-60
1955-56	1956-57	1957-58	1958-59	1959-60	1960-61
1960-61	1961-62	1962-63	1963-64	1964-65	1965-66
1966-67	1967-68	1968-69	1969-70	1970-71	1971-72
1972-73	1973-74	1974-75	1975-76	1976-77	1977-78
1978-79	1979-80	1980-81	1981-82	1982-83	1983-84
1984-85	1985-86	1986-87	1987-88	1988-89	1989-90
1990-91	1991-92	1992-93	1993-94	1994-95	1995-96
1996-97	1997-98	1998-99	1999-00	2000-01	2001-02
2002-03	2003-04	2004-05	2005-06	2006-07	2007-08
2008-09	2009-10	2010-11	2011-12	2012-13	2013-14
2014-15	2015-16	2016-17	2017-18	2018-19	2019-20
2020-21	2021-22	2022-23	2023-24	2024-25	2025-26
2026-27	2027-28	2028-29	2029-30	2030-31	2031-32
2032-33	2033-34	2034-35	2035-36	2036-37	2037-38
2038-39	2039-40	2040-41	2041-42	2042-43	2043-44
2044-45	2045-46	2046-47	2047-48	2048-49	2049-50
2050-51	2051-52	2052-53	2053-54	2054-55	2055-56
2056-57	2057-58	2058-59	2059-60	2060-61	2061-62
2062-63	2063-64	2064-65	2065-66	2066-67	2067-68
2068-69	2069-70	2070-71	2071-72	2072-73	2073-74
2074-75	2075-76	2076-77	2077-78	2078-79	2079-80
2080-81	2081-82	2082-83	2083-84	2084-85	2085-86
2086-87	2087-88	2088-89	2089-90	2090-91	2091-92
2092-93	2093-94	2094-95	2095-96	2096-97	2097-98
2098-99	2099-00	2100-01	2101-02	2102-03	2103-04
2104-05	2105-06	2106-07	2107-08	2108-09	2109-10
2110-11	2111-12	2112-13	2113-14	2114-15	2115-16
2116-17	2117-18	2118-19	2119-20	2120-21	2121-22
2122-23	2123-24	2124-25	2125-26	2126-27	2127-28
2128-29	2129-30	2130-31	2131-32	2132-33	2133-34
2134-35	2135-36	2136-37	2137-38	2138-39	2139-40
2140-41	2141-42	2142-43	2143-44	2144-45	2145-46
2146-47	2147-48	2148-49	2149-50	2150-51	2151-52
2152-53	2153-54	2154-55	2155-56	2156-57	2157-58
2158-59	2159-60	2160-61	2161-62	2162-63	2163-64
2164-65	2165-66	2166-67	2167-68	2168-69	2169-70
2170-71	2171-72	2172-73	2173-74	2174-75	2175-76
2176-77	2177-78	2178-79	2179-80	2180-81	2181-82
2182-83	2183-84	2184-85	2185-86	2186-87	2187-88
2188-89	2189-90	2190-91	2191-92	2192-93	2193-94
2194-95	2195-96	2196-97	2197-98	2198-99	2199-00
2200-01	2201-02	2202-03	2203-04	2204-05	2205-06
2206-07	2207-08	2208-09	2209-10	2210-11	2211-12
2212-13	2213-14	2214-15	2215-16	2216-17	2217-18
2218-19	2219-20	2220-21	2221-22	2222-23	2223-24
2224-25	2225-26	2226-27	2227-28	2228-29	2229-30
2230-31	2231-32	2232-33	2233-34	2234-35	2235-36
2236-					

FIGURE 30

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGAAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCCCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTT
ATGGAAGGCGGCCAAGTGGAAATATAAGCCCCCTTCGGGCATTCCGTACATGTGGTCGTACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAG
GATTCCGAGAATCATTGTATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAAGTCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAACGCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTGTGTTGATC
TGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
TAAAAGACCTAATAAACCTATTCTTCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE
LDTERENMKCVLGFIAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFSLVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFSLFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTTAGA
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT
 GAAAATTTTTTGAAGGAAATTTGCCTTCTTCAAACAAGGGTGTCAATCTGATATTTATGAGGAC
 TGTGTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTCCCTGTTTGTCTGGTGACTGGAGTAC
 ATTCAAACAAGAAACGGCAAAGAAGATTAAAGGCCCAAGTTCACTGTGCCTCAGATCAACTGC
 GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTTATTGTGAAATGTCCAGCAGGATGCCAAGA
 CCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG
 TACACAGTGGTGTGCTTGATAATTCAAGAGGGAAAAATACTTGTTCGGAAGGTTGTCTGGACAGTCT
 GGTTACAAAGGGAGTTATTTCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAACTACCCATCAGCTCTTACATACTCATCAT
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGG
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC
 CACCTTGCCAAGGCCATCCCTTCTGCTGCTTCTACCACCAGCATCCCAGACCACAATCAGTGG
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCC
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC
 GGATGTGAGCCTGGGACTTGTTCAAAAGAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCC
 TGGGAGATCCAACTGCAAAATTGACTTGTGCTTTTTTAATTGATGGGAGCACCAGCATTTGGCAA
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGC
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACCTCAAGACAC
 ACACGAATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT
 GTAGGTGCGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCCAAAGCCAATGGAACAGAAAGCGG
 GGCTCCCAATGTGGTGGTGGTATGGTGGATGGCTGGCCACGGACAAAAGTGGAGGAGGCTTCAA
 GACTTGGGAGAGAGTCAGGAATCAACATTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAG
 AAGCAGTATGTGGTGGAGCCCAACTTTGCAACAAGGCCGTGTGCAGAACAAACGGCTTCTACTC
 GCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCTGCAGCCTCTGGTGAAGCGGGTCTGCG
 AACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAAGTGGCTGACATTGGCTTCGTCATCGAC
 GGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGTTTGTGACCAACCTCACC
 AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC
 TGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC
 TACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
 GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCGACGGGAGGTCCTACGACGACGTCC
 GGATCCAGCCATGGCTGCCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCTGGGCT
 GCCCAGAGGAGCTAGAAGTCAATGCCACTCACCCGCGCAGAGACCCTCCTTCTTTGTGGACGA
 GTTTGACAACCTCCATCAGTATGTCCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC
 AGCCTCGGAACTGAATTAGAGCAGGCAGAGCACCAGCAAGTGTGCTTTACTAACTGACGTGTT
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC
 AAATGTCTTGTTATTATTCTTTGCCATCATGCTTTTTTCATATTCCAAAACCTTGAGGTACAAAGA
 TGATCACAAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTCTGGAGATTTTACAT
 TTTGACAATTGTTTTCAAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG
 AGCTTTTGTGAGATTTTTAAGTTGTTATTTCTGATTTGAACTCTGTAACCTCAGCAAGTTTCAT
 TTTTGTGATGACAATGTAGGAATTGCTGAATTAAATGTTTGAAGGATGAAAAATAAAAAA
 AA
 AAG

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPGAAFOKP
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATHTNLKTHNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLPVLRVCDTDRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARHDSFF
VDEFNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
CAAACCATGTCTTTTTCTGTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTAATTAAGCATGGAAT
ACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC
GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTCACCCGAGTGTA
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCGAGTA
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTCACTCCTGAGTTTCTTTGTGATGTGGTAC
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTTA
CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAACCTGCTCTCATCAAATCCATTTCTGGTCATTC
TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC
ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
ACCTGACCTTGAAACCATTTATGGCATTGAGGTGGGTAAGTGAAGTTTGCCCCAATGCCAAGTACGTAATG
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
GAAGTTTTTCACAGGTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAATGTCCAGAGAT
TTGTGCGCAAGGATCTATGAAATGATGGGTACGTAACCAATCAAGTTTGAAGATGTTTATGTCGGGAT
CTGTTTGAATTTATTAAAAGTGAACATTCATATTCAGAAGACACAAATCTTTCTTTCTATATAGAATCC
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
TGGCAGGTGATGCTAAGGAACACCACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAG
GATACCTTGTGAAAGTGTAAATAAAGTAGGTACTGTGGAATTCATGGGGAGGTGAGTGTCTGGCTT
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTACACTTGTGATTTATTAGTCAGG
CCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTACTGAGTTATAAGCTCA
CTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA
CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTTACAGTTATT
ATTATTTAAATTAAGTCACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAAGGATAG
TGAATCATTCCTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
TTAATGTAAAGTCATAGGTCAATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWSWGYEVLTFLLGQEAEEKDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYFPKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLKVNHIPEDTNLFYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAAGCTGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCCATGTG
GCCAGGTTCTGCGAGCCCCAAGGGGTCAGATTTTGTGAAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTATGC
TAAACCTGGGTTTGTCAATCCAACTAAGATTTGTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGTATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCATCCAGAGCATAG
GATCCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTGACGGTTTCCATGCCATTTATGAGGAGATCAGAGC
ATGCTCCTCATCCCTTGTTCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGGGACGCCATGCTAAAATGGCACCGTGGTGTCTTTCTTTGTAACTCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAAGGAAACAGCCATCTGCATAAAAGCTGCCGA
GAACCAAGATTTAGACCTGGTGAGAAGGAGAGTCTTCCGATGCAGGTTAGTCAAGGGAGACACATTACACAGCATAT
ACTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTCCCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCGCCCATGGG
ATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGGGGGCACCATCTGCATCCCTATCTGCGGGAAAATGAGAACATCACTGCTCCAAAGA
CCCAAGGGTTGCGCTGGCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCTACACAGGGAGC
GTGGTTCCTAGTCTGACGGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATCTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACCCATCCTGCTTGATGCTGACATCGCCATCCTGAAGCT
CCTAGACAAGGCCGCTATCAGCACCAGTCCAGCCATCTGCCCTCGCTGCCAGTGGGATCTCAGCACTTCTTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCATGACAGACAGGAGGCATCGCGGCTGTGCTTCCCGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAGGTGCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCGCTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACCTTGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCCTTTGAGGCTCTCAAGTTCTAGAGAGTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTT
TGTTGATACAGGCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTAATAAAATAAGGGTTGGCTTCT
GAACTACAAA
AAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII
KRVCGNERPAPIQSIGSSSLHVLFSHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSGNE
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMPQVQSRETPLHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGCTTCTGTTGC
TGGTCTTGCCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATTACAGAACTCTGTA
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCAAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCTTGGCCTAGACA
ACCTGCTACGTGCTCCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGAGCAACCGAACTA
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGGGCAGGGAATTTCTGAAACACCACTGCCCTGAAG
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCAGTGAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACCTACGCTGTGCGTCTCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAAACAGAAGTTCCGCA
GCAGGAACAATGGACAGGCCCCGGATGCTACAGACCCCGAGATGACAGCTTTTATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGGAAATAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAGTGGCGCTCATCTGATTGAGGCCAGTGAAAGACGTGTTACCTCGTGTCCCGCCAGGTTGGCGAGC
GGAGCCCTGACATCTTTGAGGAAGCCGGTGGAACAGCAATGGCAGCTGGTCCCGAGGGCCAGGGGAGAGGAGCAACA
CTCCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATGATGTTGAGCCCGGAGGAG
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC
GGAGTGAGGAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCGAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTACTGGTCCCATCCT
GGGTGATGTGGCTGGAATTACCACGGTGCTTGTATACTGTAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAACAAACCTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATAGAAATCAATGATGGGTGAGGAGGAAAACAGAAAAATCACAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTGAGTTTTTATATTAAAGAAAGAAATACATTGTAATAATGTGAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATTCCAAAAAATTAACCTACTAGTTTTTTTTCAGTGTGGAGATTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAGCCCTAAACAACTAAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTTACAGCT
AAAAATATTTTTTAAATGCAATGCTGAGAACGTTGCTTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRSQDGC PDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSRSFKKINR
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
GGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQ LGIKLVRKVDEPGVFI FNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESA AHLIQASERRVHLVVS RQVRQ RSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR
IKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
SDWSPSWVMWLELP RCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
CACCAGTAATACTTCTGTTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
GACAACTGTCTTCTGTGTCTCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGTCTGGAA
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
TAAAAAGTTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAATACTGGGGAT
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTGAGTAGTTGTTCTTATAAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCAATGACCC
TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTTGTATTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTCAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAAGTTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGTGCCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

FIGURE 42

MGFNLTFLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWGGE
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCAACAG
ACGGGACAACCTTGCAAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCCGTCCCCTCCC
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTGTTT
TCCAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 44

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCCTCCTGTGTCTCCTGTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYLWQLTGAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFFDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVS RNFS PILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTtaggtctattgcttgttggaattctggaggtcctgtttgggct
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLLVLLLVLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNPSNSNANCEFSL
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCTCGAACTGTGA
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCCTGGGAGGCCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTT
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCKYKS
SQKQHSPVPEKAIPILITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGAGGCTGGCCCCCTGCAGAG
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA
GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG
GTGCCTGGCCACAGTGGTGCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
CATAAACC CGGTGTGAAAAGCCAGGGAATGAAGCCCCGCGGGAGCGGGGAATCTGGGATTCAGGG
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
GGTGGAGTCAATACTGTGAACCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA
GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCAGCTCCCTCCTTAA
AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA
AA
AA

[illegible]

Signal peptide:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Cell attachment sequence.

APP ID=10063532

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTGCCCCGCATCCTGGCTTGACCTATGCCTTCTATAACAACTGCCGCCGGCTCCAGTGTTTCC
CACAGCCCCCAAACGGAACCTGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGCGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGGCCAGTGAATATATTGCCACCAT
CTTGAGGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTCATCCGGGAGCGGCGTCGCACCTCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGAGGGCCATGACACCAG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCCTTCTCCGCA
GGGCCCAGGAACATGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGCGGTTGAT
GCTGCTGCACTTCCGGTTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCACTGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTATGAATAAACGGTGTGTCAAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG
LITPTEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGE GILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTTGGCCGTGTGTCTTGC
ATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
GTAACCTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTGCTT
GTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGAATCTTCCTCATGTACCTGTTTCCTC
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTCAGCAACAGCAAAAAAAAAAAAA
AA

FIGURE 56

MGFVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCILQSLALTWYLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

MGFVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCILQSLALTWYLSFIPFAR
DAVKKCFVCLA

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCAGCCAGCAGGCCGCCAACATGCTCTGTCTGTGCCTG
TACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTCATCCCCCTCCAGGAATTCTCCACCTACCGCCAGTGGAGCAGAAAATTGTACAAGCT
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCGGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATCTCAAGAGCATGGATAAAAACGGCAGCATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCTCCACCCCGTGGAAAACATCCCCGAGATCATCTCTACTGGAAGCATTCCACG
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA
CACCTGGTGGCAGGAGGTGGGGCAGGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCCATGCTCCCGCAGCAACAACATGGGCATCGTTGGTGGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGG
TCACCTCTGGCGGGCAATGGCATCAACGTCCTCAAATTCGCCCGCAATCAGCCATCAATTCATGGCCTATGAGCAG
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC
ATCGCCAGAGCAGCATCTACCCCAATGGAGGTCCCTGAAGACCCGGATGGCGCTGCGGAAGACAGGGCAGTACTCAGGA
ATGCTGGACTGCCCGAGGAGATCCTGGCCAGAGAGGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTG
GGCATCATCCCTATGCCGGCATCGACCTTGCACTACGAGACGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTG
AACAGCGCGGACCCCGGCTGTTGTGCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGGCCAGCTAC
CCCCGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCCTC
TTCAAACATATCTGCGGACCGAGGGGGCCTTCGGGCTGTACAGGGGGCTGGCCCCAACTTCATGAAGTTCATCCCA
GCTGTGAGCATCAGTACGTGGTCTACGAGAACCTGAAGATCACCTGGGGCTGCAGTCCGGCTGACGGGGGAGGGC
CGCCCGGCGAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACCT
AAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGACCCGCGAGGGAGGGTGGGGAGAGCTGGCAGGCCAGGGCTT
GTCCTGCTGACCCAGCAGACCCCTCTGTTGGTTCAGCGAAGACCACAGGCATTCCTTAGGGTCCAGGGTCAGCAGG
CTCCGGGCTCACATGTGTAAGGACAGGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT
TAGTTCTTCCATTTACCCTTGACGCGAGCTGTTGGCCACGGCCCTGCCCTCTGGTCTGCCGTGCATCTCCCTGTGC
CCTCTTGCTGCCTGCCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCACCCCTCGTCCAATCCC
ATAATCCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCCCTGACTTCCCAACCTACAGCATTGACGCCAATTTGGC
TGTGAAGGAAGAGGAAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG
CTTGGGAGTCAGGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGGGGCGAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAGGTGTTGGAGGCCCTTAATTATGG
ACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTCCAACCCAGCAGGGGGCGCAGC
GGGACCAGCCCCACATTCCACTTGTGTCACTGCTTGGAACTATTATTTTGTATTATTGAACAGAGTTATGTCCCT
AACTATTTTTATAGATTTGTTTAATTAATAGCTTGTCAATTTCAAGTTCATTTTTATTATATTTATGTTTATGTTGTT
GATTGTACTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAGGGGGGCTTGGGCGCTGCACTCACATCT
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAAGGCAGCAGCCCTGGCTCCTTTCTTTTGGCAG
GTTGGGGAAGGGCTTGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGCGGTGGAGAGAGGGGAGGAACCTCAAT
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG
TGAGGTGCTCTCACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCTCCAGC
CTTCTGCTGCCCTTGTCTAACAATGCCGGCAACTGGCGACCTCACGGTTGCACTTCCATTCCACCAAGATGACCTGA
TGAGGAATCTTCAATAGGATGCAAGATCAATGCAAAAATGTTATATATGAACATATAACTGGAGTCGTCAAAAAG
CAAAATTAAGAAAGAAATGGACGTTAGAAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTTCAAGCTGAAAAA
AA

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQIVQAGDKDLG
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWVRLVAGGG
AGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQAQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVTRMQAASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCTGATAT
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGTGCTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCAGGTGTGAGGCTCCCCGATGGTTCCCC
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACCTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
GTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAAATAATTCATGTGAAC TAGACAAGTGTGTTAAGA
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTATGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCCGAAAGTCTATCCCAACATATCCACATCTTATATCCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 60

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYIMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCTGGTGGTGGTTATGGGGGTCTGCCCCTGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAATCCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCCATGGTGCAGCCACCTCCAAGTTCCACGGTGCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAGAACCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGG
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAAGTGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTGGATTCTGCCACACCCATAAAT
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYQGGAPPNVDPEAYSWFQSVDSH
SGYISMKELKQALVNCNWSSFNDETCLMINMFDTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDEFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCCACCTGCAGGAGGTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCTGGGGGA
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCGCTGATCACCCCTGGGGTACCCTGAATCCCAGTG
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCCTCCTGGAGTCTCCGC
CCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTGTCAGTG
GGGCTAGAGCAGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGLLLVLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSQVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRSNSLGAGGKILSORP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMPHPEGIWGINNQPPGTSWGNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGCCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGPLVLVLLLTILGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCTGCGGTTCTGCTGGCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLG L L L L A L G L P F L L A R W G R A W G Q I Q T T S A N E N S T V L P S S T S S S S D G N L R P E A I T A I V V F S
L L A A L L L A V G L A L L V R K L R E K R Q T E G T Y R P S S E E Q F S H A A E A R A P Q D S K E T V Q G C L P I

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTCTGTGCCTGCTGCACCAG
TCAAATACTTCCTTCATTAAGCTGAATAAATATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAAACATGAA
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA
GAATCTGGAGAGAAAGGCGAATACATTACATTCACCCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA
CCAGGCAAACTGTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACCTGTATGGAAAAGATTGTCAATTCCTT
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAA
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAACATAAAGTGCAATTTTGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTTAAACACCATACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAAGACCGCCTAAATCGAATGAATCAAGCAGCA
AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
AATAAGCTAATCAAATAAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAATTAATATGCAATTTAGGTGATGGAGAGCTACATCCCAACTCGATGGATCCGAAGTA
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTCTTGTATTGATGAAGTGAACAAAAGTGGGGCCATTGTTCAAT
TTTATGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT
TCAGATGAAGCTCAGAACAATGGCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATCTGATCTCTCCAGAA
TCCCTTCAGCTCGAAAGTAAGGGATTAACTAGTAATGCTGGATGAACGACACTGTCATAATTGATAGTACA
GTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCCACTGGAACA
ATAATGGAAAATTTACAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAAGTGAAGGTGGGCACT
TGGGCATACAATCTTCAAGCCAAAGCGAACCAGAAACATTAACATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT
GTGCCTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAACAGTTTCCCCAGCCCAATGATTGTTTACGCAGAA
ATTCTACAAGGATATGTACTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
TTGGAACCTTTGGATAATGGTGCAGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAAGTTCGGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATTACGGCCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAAACCCGCAAGACCTGAAATTTGAT
GAGGATACTCAGACCACCTTGGAGGATTTAGCCGAAACAGCATCCGGAGGTGCATTGTGGTATCACAAGTCCCAAGC
CTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTCATGAGGATAAGATTATTTCTT
ACATGGACAGCACCAGGAGATAATTTTATGTTGGAAAAGTTCAACGTTATATCATAAGAAATAGTGCAAGTATTCTT
GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTACCAAAAGGAGGCCAACTCCAAGGAA
AGCTTTGCATTTAAACCAGAAAATATCTCAGAAGAAAATGCAACCCACATATTTATTTGCCATTAAAGTATAGATAAA
AGCAATTTGACATCAAAGTATCCAACATTGCACAAGTAACCTTTGTTTATCCCTCAAGCAAACTCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTGATAAAAAGTCATAATCTGGAGTTAATATTTCTACGCTGGTATTG
TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC
AAGTAGACCTAGAAGAGAGTTTTTAAAAAACAAAACATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT
GTGTGATCATAAACTCATAAAAATAATTTAAGATGTCGGAAGGATACTTTGATTAAATAAAAAACACTCATGGATA
TGTAAAAACCTGTCAAGATTAAATTTAATAGTTTCATTATTTGTTATTTTATTTGTAAGAAATAGTGATGAACAAAG
ATCCTTTTTCTACTGATACCTGGTGTATATTTTATGATGCAACAGTTTTCTGAAATGATATTTCAAATTCATCAA
GAAATTAATCATCTATCTGAGTAGTCAAATACAAGTAAAGGAGAGCAATAAACCAACATTTGGAAAAAATAAAAA
AA

FIGURE 70

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTASTYLFE
ATEKRFFFKNVSIILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
RVYKCGGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRILNR
MNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNQGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRLPLNRAAYIPGWVVNGEIEANPP
RPEIDEDTQTTLDEFSRTASGGAFVVSQVPSLPLPDQYPPSQITDL DATVHEDKIILTWTAPGDN
FDVGKVQRYIIRISASILDRDSFDDALQVNTDLSPEANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSANIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGAAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGCAGGGGTGA
CAACAGGTGTCTATCTTTTGTATCTCGTGTGTGGCTGCCTTCTTATTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTAGCA
GTGCTCAGAAGTGACTTGCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCCTCTTGTCTGTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCACAGGGAAGCCCTTCGCTGGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCGCCGGGGGCTGCTTGCCTGGATTCCCGGGTGCTG
GTTTTGCTGGTGTCTCTGTCTGTGCTATCTGTCTGTACATGTTGGCTGCACCCCAAGGTGACGAGGAGCAG
CTGGCACTGCCAGGGCCAACAGCCCCAGGGGAAGGAGGGGTACAGGCGCTCCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG
CCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGGAGCCATTGAATCAGCCTTGGAGACCTGAACAATCCTGCAGAGAACAGC
CCCAATCACCGTCTCTACAGCGCTCTGATTTTCATAGAAGGGATCTACCGAACAGAAAGGACAAAGGGACATTTGAT
GAGCTCACCTTCAAAGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTTCGACCATTCAGCCCCATCATGAA
GTGAAAAATGAAAAGCTCAACATGGCCAACACGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAAGTTC
CGGCAGTTTCATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAACACTTCCAAGCTGCCAATTCAGGAATTTACCTTCATC
CAGCTGAATGGGAATTTTCTCGGGGAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGGAAGCAACGCTCTCTC
TTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAG
GTATTTTATCCAGTTCTTTTTCAGTCAGTACAATCCTGGCATAATATACGCCACCATGATGCAGTCCCTCCCTTGAA
CAGCAGCTGGTCATAAAGAGGAACTGGATTTTGGAGAGACTTGGATTTGGGATGACGTGTCACTATCGGTGAGC
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGAGAGGATGTGCACCTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAGGCCATGAACGAGGATCCACGGCCAGCTGGGCATGCTG
GTGTTTCAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGCAAGTAGCAAAAAAAGACTTCCATAAA
GAAGGATTTGGGAGACACTTTTCTTTTCTTTTTCGCAATTAAGTGAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGACAAAAGAAATGGACTGATGGGTGAGATGAGAAAGCCTCCGATTTCTCTGTGTGGGCTTTTACAACAGA
AATCAAATCTCCGCTTTGCTGCAAAAGTAACCCAGTTCGACCCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTGTG
AGATTATAAGCCTAATGGTGTGGAGGTTTGTATGGTGTTTACAATACACTGAGACCTGTTGTTTGTGTGCTCATTGA
AATATTTCATGATTTAAGAGCAGTTTGTAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAATATCAGAAGGCAGGAGAGGATAGGCTTATTATGATACT
AGTGAGTACATTAAGTAAATAAAATGGACCAGAAAAGAAACCATAAATATCGTGTCAATTTTCCCAAGAT
TAACCAAAATAATCTGCTTATCTTTTGGTTGCTTCTTAACTGTCTCGTTTCTTTTCTTTTATTTAAATATGCACT
TTTTTCCCTTGAGTTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTAC
ATTTTTATATTTTAAAGATACCTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAATTTGATGCCATAT
CCAAGGACATGCCAAATGCTGATTCTGTGAGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACT
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGCAACTGAACACTGGAGGAAAGAAATGAC
ACTTCTGCTTTACAGAAAGGAACTCATTCAGATGGTGATATCGTGATGTACCTAAAGTCAAGAACCATTTT
CTCCTCAGAAGTAGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACATCTCTTTTC
AAAACAGGGTGTCTCCTGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATG
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTGTCTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACTGAATTTTAAATTAAGCAGTTTCACTCAATCACCAGATGCTTCTGAAAATTCATTTTATACCATTT
CAAACTATTTTTTAAATAAATACAGTTAATACATAGAGTGGTTTCTTATTCATGTGAAAATTTATAGCCAGCACCAG
ATGCATGAGCTAATTTCTCTTGTGCTTCTGTTGCTCACAGTAACTCATTTTAAAGCTTCAAGAAC
ATTCAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTGTTGACTGGTAGTTTATGAAATTTAATTAACACAGG
CCATGAATGGAAGGTGTTATGCACAGCTAATAAATATGATTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN
TLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYPVLF
SQYNPGIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR
KYLHSNLIVVRTPVRLFHLWHEKRCMDLTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

[illegible]

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYDSDSYDSLSEAAERPOGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLEFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCCLLLAVYFIARKIRKKRLNRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTGACAGCTCC
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACAGTGGAGTCCTTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCATATCTATTACCGTGTTCCTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
TCCCCAAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA
TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGCTGGCCGTTTGTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGHLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYGNFDFKRFVPAEK
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPDKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLLSQA
ALAVLGPQTLQYSYTPQLQDLDPQAQHTDSEEGPEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCCTCAGTCCCCTGCACTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC
ATCTGGCTGAAGGTATCAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
CCCACCCGCTGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACCTGCTGTA
TAAGCTCTCCTTCTGGTGAACGCCCTTAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCTGTTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTGAAGG
CCTTGGGATTCGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFLLCGLLAATLIQATLSPTAVLILGPKVKEKLTQELKDNATSILQQLPLLSAMREK
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGLIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLENQNGKLRSQVPSLVKALG
FEAAESSLTKDALVLT PASLWKPSPPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAATTGTGGGTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCGCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGGAGGCCCTCCTGGGATTC
ATTCTGTTCCTGGAATCTTCATGGGATCTTACGGGACTTCTACTCACCAGTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAATACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVGYYLGLLGLLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNYSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCT
GCCCACGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
ACCAGCGGCCTGACCCTGGGGAAGGATGGTTCCCGAGGTGAGGGTCTCTCTCTCTGCTGGGA
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCTCCACTGTCCGCCT
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCTGCCCAACCAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCC
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
AGAGGGCCGGGACCCCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCCTGCCGTACCCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGG
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCACGAAGGTCCT
GGAACGTCTTCTAGCCAGACCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
TAAGAAGTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHEL
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGKTY
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKAVAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGC GGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTGAGCACTGGGCTCAGTTCCCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTGAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTGTGCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACCTTTTTGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATAATCCAGGCGGAACCTGGACTG
GAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGAAACACGCAGTGGAGTGACTCTGGATCCAG
AGACGGCTCACCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAAACATTA
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCT
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGGTCTTCTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGGTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAACTCCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGCCTCTGCAATCCCAGAGACAAGCAACAG
TGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGSTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSQWQVFGDPKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNDRMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEALRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF
TRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTSNSSESSQATTPFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCT
GCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGTCATGTGCCCTGCTCCTTCTCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAGGCACCTGGAGTCCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTGTCACTCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTACTCAGGGGTGGTCCGGGGAGCTGGAG
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTGTAGTGAGGTCTGCAGGAAGAAA
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTT
AGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAG
CTTCTGCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTTPMISWIGTSVSPDPSTTRS
SVLTLPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPQNLTMTVFQGDGTVSTVLNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVS LQSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE
DANAVRGSASQGPLEPWAEDSPPDQPPASARSSVGEGLQYASLSFQMKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTIVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIPIVVYDFGDAQKTASYSPYQOREFTAGFVQFRVENNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCT
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC
AGCACCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT
ATTCGAGCGTTGGGAGTGCACGTATTGGTACATTTTGTCTTCTGCAGTGGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAGAAACCCTTCTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACIPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV
TVFGLKKKPF.

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTACCTAAGTCCCGCCCCATGGCCAATTCCTCTCTAGGGCTGCT
GGCCCCGCCTGGGGAGGCTTGGGGCATCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCC
CACCCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTAC
CATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTC
AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGTGAGCATGG
CATGAGGCTGAAGTGGAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGTTCTCCCGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGGCCGAGAGCATGTGCTGGATCTGTTT
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGAGCTTCTT
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTGGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAATTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTTTCTGGTGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAFGPALALYVFTTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLGP GTVG I HGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRS LKLCLLCQDKNFLLYNQRSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAACTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAAC
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
CAATTTTTGTACACAACCTGGAGCCCAGGGCACATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCAGG
GAACCCAGCAGGCCGCCTCCCAACTCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGAAAAC TGAAA
AA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTILGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLLIHSLEFPGGILPTSQAGANPDVQDGSLPAGGAGVNEPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCATG
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCAAGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCAGAAAACCTATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTGTGAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTCACCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGCTGAGCCGGGTACCAGGCTGGCATCCCCCTTCTCTTCTTGGAGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCAGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAACTCTCCATCATAGAGAGACCTGGGTGT
 CCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGCACCACATGGCCCCAGGTA
 CACTGGAGTGGGGGTGATGTGCACTATCACTGGAGAGCCATCCCCGGGACCCCTTTGAAGTGAA
 TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAATTCCTATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA
 ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGCTGTGAAG
 TCGAAGTCGCAGTCACAGATATCAATGATCAGCCCCCTGAGTTTCATCACTTCCCAGATTGGGCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
 CCTCGAGCCCCGCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTGCCACCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTCTGCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATTTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGCCCTGCATTGGGTGGAGCCAGT
 GAACACATAATCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTTTCAGTGAT
 CGTGTGTGCTGCAACGTGGAGGGGCAAGTGCATGCGCAAGGTGGGCGCATGAAGGGCATGCCCA
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTC
 ATTTTACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT
 GAAGGGCACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
 TCCCCCTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCACTT
 TATGGACTGCCCATGGGAGTGTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSPQALPKAQAELSVEVPENYGGNFPLYLTKLELPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQFVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDGQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRIMDFAIERGDTEGTFGLDWEPDSGHVRLRLCKNLSY
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTLRFSLVNDSEGLWCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTIVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCCTG
AGTCCAAGATTCTTCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
TCTCTTACACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAGAGACAGATGAAGATGCAGAAAGGAAATG
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCATGAGACTAGCACC
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
GCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCACCAACT
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCA
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC
AGTGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAAACACAGCCAC
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAC
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
ATGCACACAACTTCCATAGTGCACTCTACTGAGTGAAGGCAAGCCTGGTGGGTCCCTGGT
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAAGTGGTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
CCCAAGACCTGGTTTCTTTTATTCTATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA
AATCTTGAAGAAGGTATTCTCTACCTTTCTTGCTTTACAGACACTGGAAAGAGAATACTATAT
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTTG
CCCCGGGGTGGGTATCTAGCTCTGAGATGAAGTCAAGTTATAGGAGAAAACCTCCATGCTGGACTC
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSTANTGSSVSSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFRRPVSSI
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTACAGGTG
GGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGATGGAAAGGGATTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGAAGCATTT
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCCCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT
GATTATACTGGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCTATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGTTGGTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTCGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACAACATTCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTCGAATATTTCTTACT
GCCATCATTATTTGTAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTTAATCTCTGAATGAATTTTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

FIGURE 102

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSI FMLS P
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCMLRYSYLRLKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP
LQLLI FPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHL LQGDFPREIH FHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
LEIIE LACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA
GTTTGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCAGCCACAGCCAAGTGGAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAAGTGTAAACCATAGAAAAGCTCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTTGTCTCCCAACAATGGGTATTGGGTCCCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCCAGCACCCCTCCTACAGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTCAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTT
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACACTACAGGTCCATATCC
CTCATTAACACAGACACAAAAATTTCTAAATAAAATTTTAAACAAATTAACATAAATAATTTA
AAGATGATATATACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAAATATTTAAAT
ATCAACCAGTGAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLSFYELVSGWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCCCTGGGTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA
CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGA
AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
ACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
ATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA
TGACTATGATATTTCTCTTCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCT
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTG
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTG
GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
ATAAACTGTTTGCTTGATGCATGATTTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTCTGCCA
GATCAACTCTGTCATCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTCAATTGTTCTCTAGAAGTTTGTGAGAATTTTGACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCCTCAGCTCCTCTCATTTTCAGCAAATATCCATTT
TCAAGGTGCAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGAATATTAGAAATGATCATATTCAATTATGAAAGGTCAAGCAAAGACA
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAAGGAAGTCCAGAAAGAAGCCAG
ATATATCCTTATTTTCATTTCCAAACAATACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSSGGLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG
 CCCCAGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGCCCCAGC
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
 ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTACGCCCTCAA
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTCCT
 GTGGTTCATCCGGTCATGATTGCTGTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTG
 TGAACCGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGTTTGCTTGTCAATTTCT
 GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTTATGGTTCAGTACAATGGTCA
 GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
 TGCTTGGAAATTTTTTTCAGAGAGATTAAAGTGTGCTGTTGAGTAGTATATTTCACTGACTGGTTGG
 AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAA
 CAGGCCCCACCGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCCCTT
 TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG
 ACAGACCAATGATGTCTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACT
 GTTGAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAAACAGCTTTAATACACACT
 TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACT
 TGTGAATTTTTGAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAATGTTGCCATAAAA
 TAACACCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTC
 ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCGCCA
 TCCATGCAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT
 ACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAGAGCAAGCTAACACAT
 TGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT
 TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGCTGTATAGCATCATT
 ATTTTGTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGCTGGGCTTATATTACACATATAAC
 TGTATTTAAATACTTAACCACTAATTTTGAATAATTACCAGTGTGATACATAGGAATCATTATTC
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGA
 AAGGACTTGTATGCTGTTTTCTCCCAATGAAGACTCTTTTGACACTAAACACTTTTTAAAAA
 GCTTATCTTTGCCCTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCACAGAAAA
 TAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATT
 CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTTACAA
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGATTTTGTATTAT
 TTCTCAGAATATGGAAAGAAAATTAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREP GTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGATAAAGCCCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTCCAGTGTTCTGGCAGTTGGTCCAGAAGGATGCTCCATTCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTACCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAACTGCTGTCTCTGGAACACCACGGTGGAACTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCAATTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATACCAGCGAGTGCACATGCCCTCCAGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCCTACCGCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCCTGGTGTGT
CTGAGGATAACCACTTGCCAAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACGACGAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCCGTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT
CATGAGCCGAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC
TTGGAAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTTCTGCACTGCCGGGTTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTCTAAGAACATCTGCCAACAGC
TGGGTTACAGACTTCACACTGTGAGTTCAGACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA
CAGGTACAGCACTGCTGAACAATGTGGCTGGGTGGGTTTCATCTTTCTAGGGTTGAAAACCTAACTGTCCA
CCCAGAAAGACACTCACCCATTTCCCTCATTTCTTCTACACTTAAATACCTCGTGTATGGTGCAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTCAAGTTACAAACCTAGAAAAATTAACAGTTACTGAAATTATGA
CTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGTATCAATAAAACAGTATATAATTTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLQLEDSQGPFLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGETHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNIIPRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYLLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
GGTTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCCAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
AGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCAGACAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCACGCTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA
GCCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGCAG
CTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAGACAAATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTTCTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGTGTCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCCGTATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTCAGTGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCCTCGCAGCCAGAGGCGCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAGCC
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
AAAA

FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGEEASVDSWPWQVSIQYDKQHVCVGSILDPHWLTAAHCFRKHTDVFNWKVRAGSDKL
GSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQDSSGGPLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAAC TGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC
TGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCACCTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGACAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAAGGGATTGACAAGCCCGAAGATTTTCATAGGCGATGGCTCCCCTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTTCATGTCCTGCACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATATGGGTGAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAAACATG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA
TGGTTATTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKEGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:
amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAAGTGAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCATGAGGCATCTGGCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTLLIVLFWGSKHFWPEVPKKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTTFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGCGGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCTCCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAACATGCTGGTGAATACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGGGCTGGGTGCGTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAGAAGAAACCAACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCACGACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGTCTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATCCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCAAGAAAACCTTTGAAAGGAAA
GAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATAACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCCTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCAATGCCTCAGTGGAGAGTGTGGCCTTCATT
GAAAACAACATCGTGGTTTTTGAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGTCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATA
ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGAGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCAACCGAGCG
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAGCCATGCAAATG
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGCAGATGAGATA
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTTCTCC
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
TTTATAATGAAGATTAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAAGTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
CTTGTGTATTAAATTAACATTTTTAAAACGCAGATATTTGTCAAGGGGCTTGCATTCAAACGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
AAAAATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA
TGTCTTGGTTTTTCATTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACTT
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTCCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAAACTGTAAATACTGTATTTTCTGTTTATCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
TATACATTTATATTAATAAATTGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK
IYDSL LALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLVLPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCTCCAGCTCCGCGCTGCCCCGGCAGCC
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCCGGATG
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTGGACACCCAACCTAC
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGTACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACCTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTAA
AAAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAQVPGR
DGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGSLPIEAIYLDQGSPEMNSTINIHRIS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTTA
ACCGCCCCCTCCCCACCCGCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATTTATTTGTTCTTGGAG
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
TCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCATGCAACTG
GCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACCTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAAATGAATACGCAGACTCAAAGA
GCTGATTCTTAGTTCCAATAGAATCTCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT
TACGGAACCTTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA
AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCCTTACTTGCACTGGAATAAAATCAGTGT
CATAGGACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
TCGAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAACCTGGCTGAAAAGTT
TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACCTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
GGCTCTCCCAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT
TGCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
CTACGTGTCTATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTTATGTA
GATTATAAACCCACCAACACCGGAGACCGAGATGCTGCTGAATGGGACGGGACCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTGTGATAAAAAGAGCTCTTAAAGCT
GGGAAATAAGTGGTGTCTTTATTGAACTCTGGTGAATCAAGGGAACGCGATGCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCCGTTTGTAGTGCATTATAATACT
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGTTTTAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAATGTGCGATTT
GTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDSLQNQLHSLGSEQFRGLRKLLSLHLRSNSLRITPVRI FQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCGGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCCTTTGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG
AAAACCATTCGATTTTCGTGGTGTACATCATGCATTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFGESEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMQMEGKRKLEGGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTPVKHYLVLTNPLEDNIMTHGLSSSLCSGLVASILGTPADVIKSRIMNP
RDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGFLPSWLRMTPSWMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCCATGGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGACTTTGATCCCCTACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCGTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCCTCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGTGCCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCTGGCCAGTGGATTTCAITGGTGATCATTAAGAAAGAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININSMGHRVPLSVTHFYATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTTAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATGAGGAACTGAGAAAATTAATTTCTCATGTATTTTCTCATTTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAAC TGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTTATGATTACA
GGCGTGAGCCACCGTGCCCTGGCCTAAACATTTATCTTTCTTTGTGTGGGAACCTTGAAATTAT
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAATGACAGGATTCGTTCTTAATTTCAATTAAATAACACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFD CGPFRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGHGTLGESPMPPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACAACCAATAAATAATGCTGGGATTCTTTCAGAT
TTGAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCTTACCAACCT
CCCAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
AAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAATTCCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG
GTCTCACTAGTCTAAAACGCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCAGAAATTCCTGACTGCTGCACCAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTCTGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTACACCTCTGATACCATTCAATCTCTTGAAAACCTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTC
CCATGGAACACGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTT
CGAATGTACAACCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTACC
TTTGGCTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTCTTGCTTTAGTGTGTTGGTATG
TTTATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAATCAGGGAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCATATTTCCCTCAATGGAATGAATCTGT
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTGGGTTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRITITYDSLSKIPYL
EELHDDNSVSAVSIEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAGQGWPAFVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSYPKYVCMVPMETSNLYLFDETPVCIEETETAPLRMYNPTTTLNREQEKE
PYKPNLPLAAIIGGAVALVTIALALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCAGGCTTCTTGGCA
GCCCTGCCGGGCCACTTGTCTTCATGCTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCCTTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCAGCTGACCCTCCAGCCCCG
GTTTTGGAAGTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTAACCCACGTTCCGGC
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
GACAGCAGCGAGCCCTGCGGCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
AGGCTACTGCCTGTCCCACCACTGCTCTTCTTCTCTGGGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGCCATCGGATACGCCTACCCACCCGGGACATCTTCATGGAAAACATCATGTTCTG
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTCAAGC
AATTCTCTTGCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCTTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCCTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCTCTCATCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAAAAA

FIGURE 134

MSARGRWEGGRRACRGLGLARAQGAERTVSSEQRPMASLGLLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQOSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQEGCFG
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSLILP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGGAACCGGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTGTCTGTAT
GAGGTCAATATTGATGTCAGTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT
ATGAACACTATACATTATGTATATTAATTAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLKTDGSEFVVDIPSGSYVVEVVSAPYRFDPVRVDITSKGKMRARYVNYIKTSE
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAAACAA
GTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCCTCCTGCCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
AACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACCTTGAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAC TAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTGCTATTTA
ATGTATTTATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGG
CTAGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTGTGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTCCAG
CCAGGAATCCTACACGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAA
AAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNGATT CATNSHSDSEL RPEIF
SSREAWQFFLLLWSPDFRPKM KASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLT IKDLRLSHAHTCHCGEEAMKKYSQILSHFEKLEPQA AVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCCGGTTCCGCATCCAGCC
 TAGCGTGTCACGATCGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
 TAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA
 CACGGAGCGGAGCCCCAGCGCCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
 GGTCAAAGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAAAAAGGAGCATCTCACAGT
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
 CCTTCTGGCTTTGTGCGAGTTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
 TAAGACAAGCAAAGCAGCTGGAAGAAAGTATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
 TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTCTGTGTGAGATTACACAGAGT
 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTAGGGCCCCAACAGCCCCCTGATTGGGCAG
 AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAGGAGAGAGA
 GACGCTTTTACCAATTTGTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
 GGGCCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAGGAAA
 CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
 ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGAC
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG
 AATGTGCCGTATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGG
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAGTCCTATTCAACCTGGGCTCCAAGG
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG
 TTCTCACCTGCTCTGCTCAGCGTCCCACAGGCAGTGCACAGAAAGGCTGAGCTGGAAGTCCCA
 CTGTCATCTCCTGGGTTTCTCTGCTCTTTTATTGGTGATCCTGGTTCTTTTCGGCCGTTACAGT
 CATTTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT
 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCCTGGAC
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGTGTCCCGACACAGGTG
 TTCACATCTGTGTGTGTCAGGTGAGATGCCTCAGTTCTTGAAAGCTAGGTTCTGCGACTGTTAC
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
 TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
 CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCTGCCACCCCAGAATGCATCCT
 GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCTTAGTCCTTGGCC
 TCGGACACCTTCATTCTGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
 ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
 ACCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGCCCTGTGCTGAGTGT
 CTGACCGAGACACTCACAGCTTTGTGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG
 CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG
 CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPHFVEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT
TCCCTATAGAAAACAACTGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGGAGTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACATAATTGTATAAAAAACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLD SGNLI AVDPKNYIRPEI
FFALASSLSSASAEKGSPI LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACAGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTATCTATTTTGCATGTGTTTGTAGATCTCAGATCAGTGTTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAACATCAGCATTTTAAGAAAAAAAAAA
AA

FIGURE 144

MLGLPWKGGLSWALLLLLLLSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLGFFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCAACATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCAC TGCGCCACCTGCTTCACAGTACTTCCCAACAACCTTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCTGGCTTGCTTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHL SAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWL MVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

[illegible][illegible]

FIGURE 148

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCCAGTCC
CGGCCCCCTCTCCGCCCCACACCCACCCCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTCTATA
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACTTGGAATTCTGGTGTAGTGCTCCCATTCAAGCTTTCCCAAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTT
TGTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAACCTACAGTGAAGACAACCTTGAGGAACCTCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTTCAGAAAAAGAAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAAATTTTTGACCCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE
RRTKTYSEDNFEELQYFPN FYALLKSIDSEKEAKEKETLITIMKTLD FVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEA AKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTCTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCACTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAAG
CCAGTGCCTGTCTGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTACCTTCTACCGGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCCGGCTGCCTACCGGGCTGGTTCCCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTGAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAAGGGT
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTGTGACTTAG
TGGGCACCTGACCACCTTTGTCTTCTGGTTCCAGTTTGGATAAAATCTGAGATTTGGAGCTCAGT
CCACGGTCTTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTAACAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCT
TAATGGTAAGTACAAGTGTACCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA
GGGTGAGTAGCTCTCCACATGAAGTCTGTCTACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCTATA
TGCTACCTTTTCCCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTGTCAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGA
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTATATATATT
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT
AGGTGATTTTTCTTTAATTCTGTTAATTTATCTGTATTTCTAATTTTCTACAATGAAGATGA
ATTCCTTGATATAAAATAAGAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAAAAATCATCTGGTAATCTTTCTCTAGAAG
GATCAGAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAACTCAGTCTGTGAGTTTATTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATAT
GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAGAGGCAAGAAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCCGGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT
CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCACCACAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAGTGTGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTGTCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
GCCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTTGGTCTAATCTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMDKSAKVLVYLHNNQLLAGGLHAGKVIKGEETISVVPNRWLDASLSPVILGVQGGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGWGNAPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCCTTATGGGGACCCCTGGCCACCAGCTGCCTCCTTCTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGCTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACCTTACCCTTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTC
CAGCCTTATATGCAGGAGGTGGTGCCCTTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAGGAAGATGGGAAGCCAAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFIMGTLATSCLLLLLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAAATAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCAGTGCAGAGGGC
TGCCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCAT
TCTTGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCCGT
TGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCCAGATGCTTGCCCCCTGTGAAGTGCTGTCTGGAGCAG
CAGGATCCCCGGGACAGGATGGGGGGCTTTGGGGAAAACCTGCACCTCTGCACATTTTGAAAAGAG
CAGCTGCTGCTTAGGGCCCGCGGAAGCTGGTGTCTCTCATTTTCTCTCAGGAAAGGTTTTCAA
GTTCTGCCCATTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCCTG
GCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT
TGTTTGTCTTACTCATCTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA
GTAGAAGTGAACCTTACAACCACTCCCCGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCAGAGTGGTGCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLDLRLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPPQTGVFPPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCCCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCAACCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 160

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVSMSRNIERSRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV
RRKHQGCVSFQLEKVLVTVGCTCPTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

AACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG
 ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT
 CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGGCAGCAC
 AGGGCCTCAGGCCGAGGTCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTTGTGTCTCT
 TGGCACTGGGCGGAGCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC
 CACTGCTCTCCGGGCTCTCTGCGGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT
 CGTGCTGTCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC
 AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG
 GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA
 TGCCCTCTCTCCAGGCCCAAGTCGTGCTCTCTCTCCAGGCCCTACCCTACTGCCCGCTGCGTCTGC
 TGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGAC
 TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTATACTCAGCCCAGGTACGAGAA
 GGAACCAACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTCAGCAGATGGTGACA
 ACGTGATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG
 GTCCAGGGCCCCCAAAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAA
 CCACACAGACCTGGTTCCCTGCCTCTGTATTGAGGTGTGGCTCTGGAACCTGACTCCGTTAGGA
 CGAACATCTGCCCCCTCAGGGAGGACCCCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTG
 CGACTGCTGACCTGCAGAGCTGGCTGCTGGACGCACCGTCTGCTGCCCGCAGAAGCGGCACT
 GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACTGGTCCACCGCTTTCTGGGAGAACG
 TCACGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCTAACCTCTGTGTTCAGGTG
 AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGA
 CGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAACCCA
 GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGAGAGTACTTACTA
 CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG
 CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG
 CTGCGCTTTCCCTCATCTCTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAA
 CAGGACGTCCGCTCGGGGGCGGGCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGA
 CTCGGGTTTCGAGCGCTGGTGGGCGCCCTGGCGTCCGGCCTGTGCCAGCTGCCGCTGCGCGTGG
 CCGTAGACCTGTGGAGCCGTCTGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAG
 CGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGTCTCTCTCCCGGTGCGGTGGCGCT
 GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCTTCC
 GCGCCTCGCTCAGCTGCGTGTGCCCCGACTTCTTGAGGGCCGGGCGCCCGGCAGCTACGTGGGG
 GCCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGACCGTGCCCGTCTT
 CACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCG
 GCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCCAGCCAGCCCTGGATAGCTACTTC
 CATCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA
 CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

FIGURE 162

MPVPWFLLSLALGRSPVVLSSLERLVGPQDATHCSPGLSCRLWDSIDILCLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDCLRLVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVVSADGDNVHLVLNV
EEQHFGLSLYWNQVQGPEKPRWHKNTLGPQIITLNTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN
LWQAARLRLTLQSWLLDAPCSLPAAEALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKIQLECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLIILLKKDHAKGWLRLKQDVRSGAAARG
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHPDAVPALFRTVPVFT
LPSQLPDLFGALQQPRAPRSGRLQERAEQVSRLQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
 GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA
 AAACATCTTGACGTGGGACAGCGGGCCAGAGGGCAGCCAGACAGGTCTACAGCATCGAGTATA
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTGAGCGGATCACCCGGAAGTCTGC
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
 GTCAGTGGGGAGGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGTCTCTGCAGCACACTAC
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTCATCCTA
 CCCCCACGCCAATCCGTGACAGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
 ATATGAGTTCTTCGGCTGACCCCTGACACAGAGTTCCCTGGCACCATCATGATTTGCGTTCCCA
 CCTGGGCGCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
 TACTCCTTCTCCGGAGCCTTCTGTCTCTCCATGGGCTTCTCGTCGAGTACTCTGCTACCTGAG
 CTACAGATATGTACCAAGCCGCTGACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT
 TCCAGCCGCTGCCCTTCATCCAGGAGCAGCTCCTGATCCTGTCTTTGACCTCAGCGCCCCAGC
 AGTCTGGCCCCAGCCTGTCCAGTACTCCCAGATCAGGGTGTCTGGACCCAGGGAGCCCCGAGGAGC
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
 CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAAACGCTGCCCTGAG
 GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTCTACGCCCCACA
 GGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
 CCTATGGGGTATGCATGGAAGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTCTAAA
 CACCTTAGGCCTAAAGGTGAGCTTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
 CCCTGGGGATTTGCACAGACAGAATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGACA
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCCTGAGACCTCAGACCTG
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGCAGTGGGAGTCCCTG
 AGGGGAATGGGAAAGGCTTGGTGCTTCTCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
 ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
 AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCCTCACCAGGAACAAGCAGCATGATA
 AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTG
 CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTTGCCAGTTTC
 ACAATCTAGCTCGACAGAGCATGAGGCCCCCTGCCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA
 GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACAGAACAACTGC
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGTCA
 TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTCATTCTCTGATAGAACAAAGC
 GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCCT
 ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAACACAC
 TGTACTGATGTCACAACTTTGCAAGCTCTGCCTTGGGTTGAGCCCATCTGGGCTCAAATTCAGC
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCCGAAGCCTCGGTTTCTC
 ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
 TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
 AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDVTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTELYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCTIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTFOPLRFIQEHVLI PVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFFPYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCMLGGLSLQEVTSLAM
EESQEAQSLHQPLGICTDRSDPNVLHSGEETPOYLKQQLPLLSSVQIEGHPMSLPLQPPSGPC
SPSDQGPPSPWGLES LVC PKDEAKSPAPETSDLEQPTELDSLFRGLALT VQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA
AGTGTGTAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCTGTGCCTGAGCCCAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA
ATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGTGTTTACAAAGATTGTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAATATATTATTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEECSMIMYRGKALEDTGPDRCRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADETDFVCFEGGRD
DFNSYNVEELLGSLELEDSPVEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRADSEDGEGA
FSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGESERTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCCTCTAGGACATACACGGGACCCCTAACTTC
AGTCCCCCAAACGCGCACCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCGGCCGAAGCGGATGCGCGCAGGGGGTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTAGAGTTCGCGGGCTGCGCCCTG
GGCAGAGGCCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGCTGCTGCTGGGCGCGCGCTGCTGCTGCCGCCACGGAGCCTTCTGCCGCCGCGTGGTCAAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAGT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCTCTCTCA
GCCTTGAGAATGAAGCAGAACAGAAAGTAAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAAACATCTGG
TGCCTGCCCAGATCTCTACCACTGGTCTGATGGAAGCAATTCCCAGTACCGAACTGGTACACAG
ATGAACCTTCTGCGGAAGTGAAGAGTGTGTGTGATGTATCACCACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCACTGGAAATGATGACAGGTGTAACATGAAGCACAAATATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACACCCATCAGAATGTGGTGTACTGAAGCAGGTATAATCCCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTGTGTTTGGAACTGTTGTTTCCAGATGCT
GCATAAAAGTAAAGGAAGAACAAAACTAGTCCAACACAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAAATACTATTGACTTGGTTCCAGAATTTTGAATTTCT
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGAATGGCTTGAATCACAAGGATCTGC
AAGATGAAGTGAAGCTCCCTTTGAGGCAAAATATTAAAGTAATTTTATATGTCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAAGCAATTCCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA
ATGAAGTGTCTAATATTTATTTTATGGCATCTCATTCTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCACTGAATTCACACACACAAATATAGTACCATAGAAAAAGTTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA
AATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTGTAGCTTAAATTAACAGATT
TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGTCTTACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
GGGTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTGTGTCGGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAGTGTAGTCTAAGGTTTCCCTAGCTGTATTAGCCTCTG
ACTATATTAGTATACAAAGAGGTCTGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAATGGGTTGG
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGTCTGAGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTCAAGAGAAAGTTGTAAGTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAACCAATAAAGAGTCTTGTGTTCTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYK MAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHN YICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKS KGRTKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217